

Best Local Similarity 100.0%; Pred. No. 23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
Db 558 AKARQAR 566

## RESULT 4

AAE19387  
ID AAE19387 standard; protein; 667 AA.

AC AAE19387;

DT 31-MAY-2002 (first entry)

DE Human single minded homologue 2 (SIM2) protein, long form.

KW Human; single minded homologue 2; SIM2; colon cancer; prostate cancer;

KM pancreas cancer; chromosome 21q22.2.

OS Homo sapiens.

PN WO200212565-A1.

PD 14-FEB-2002.

PF 06-AUG-2001; 2001WO-US024781.

PR 04-AUG-2000; 2000US-0223531P.

PR 22-DEC-2000; 2000US-0257965P.

PA (UFL) UNIV FLORIDA ATLANTIC.

PI Narayanan R;

DR WPI; 2002-227169/28.

DR N-PSDB; AAD30522.

PT Detecting cancer in tissue sample, involves providing tissue sample, and  
analyzing tissue sample for presence of single minded homolog 2 marker.

XX Claim 19; Page 56; 60pp; English.

PS The invention relates to a method of detecting cancer in a tissue sample.  
CC The method involves providing the tissue sample and analyzing the tissue  
CC sample for the presence of a single minded homologue 2 (SIM2) nucleic  
CC acid or protein, where the presence of the SIM2 marker in the tissue  
CC sample indicates that the tissue sample contains cancer. The method is  
CC useful for identifying compounds that modulate expression of SIM2 gene in  
CC a cell. It is useful for detecting and reducing the growth of cancer such  
CC as colon, prostate and pancreas cancer in an animal or mammal. The  
CC present sequence is human SIM2 protein, long form. SIM2 gene is located  
CC on chromosome 21q22.2

XX Sequence 667 AA;

Query Match 100.0%; Score 40; DB 5; Length 667;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
Db 558 AKARQAR 566

## RESULT 5

AB38971  
ID AB38971 standard; peptide; 96 AA.

AC AB38971;

DT 06-FEB-2002 (first entry)

XX Peptide #6477 encoded by human foetal liver single exon probe.  
DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

PS Claim 27; SEQ ID NO 31606; 639pp + Sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human fetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 96 AA;

Query Match 92.5%; Score 37; DB 4; Length 96;  
Best Local Similarity 88.9%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
Db 23 AKARQAR 31

## RESULT 6

AA32455  
ID AA32455 standard; protein; 96 AA.

AC AA32455;

DT 18-OCT-2001 (first entry)

DE Peptide #6492 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

KM genetic disorder.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2006, 19:02:04 ; Search time 229 Seconds  
(without alignments)  
27.728 Million cell updates/sec

Title: US-10-501-964-1  
Perfect score: 40  
Sequence: 1 AKARQANR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	40	100.0	667 1 SIM2 HUMAN	Q14190 homo sapien
2	37	92.5	80 2 Q92X88 RHIME	Q92X88 rhizobium m
3	37	92.5	516 2 Q6ZRH9 HUMAN	Q6ZRH9 homo sapien
4	36	90.0	186 2 Q5NTN3_9BACT	Q5NTN3 uncultured
5	36	90.0	562 2 Q4P8F5_USITVA	Q4P8F5 usitlago ma
6	35	87.5	135 1 RL19_XANAC	Q8PMY0 xanthomonas
7	35	87.5	135 1 RL19_XANCP	Q8PBC0 xanthomonas
8	35	87.5	135 2 Q4US85_XANCP	Q4US85 xanthomonas
9	35	87.5	167 2 Q5H389_XANOR	Q5H389 xanthomonas
10	35	87.5	469 2 Q7MX74_CHRYO	Q7MX74 chromobacter
11	35	87.5	473 2 Q4NFW2_9DELT	Q4NFW2 anaeromyxob
12	35	87.5	530 2 Q5KTI9_9BTRK	Q5KTI9 waurexilla n
13	35	87.5	599 2 Q8A6J5_BACTN	Q8A6J5 bacteroides
14	35	87.5	2472 2 Q14214_HUMAN	Q14214 homo sapien
15	35	87.5	3667 2 Q51002_HUMAN	Q51002 homo sapien
16	35	87.5	6669 1 NEBU_HUMAN	P20929 homo sapien
17	34	85.0	233 2 Q7NMC3_GLOVI	Q7NMC3 gloobacter
18	34	85.0	242 2 Q6ZB10_BURMA	Q6ZB10 burkholderi
19	34	85.0	303 1 LIFO_CHRYO	Q7NUI5 chromobacter
20	34	85.0	312 2 Q9L1D3_STRCO	Q9L1D3 streptomyces
21	34	85.0	580 2 Q82XK3_NITRU	Q82XK3 nitrosomona
22	34	85.0	716 2 Q41785_GIBZE	Q41785 gibberella
23	34	85.0	738 2 Q51J37_MAGGR	Q51J37 magnaporthe
24	34	85.0	765 2 Q8XZK9_RALSO	Q8XZK9 ralslonia s
25	33	82.5	106 2 Q5DN15_9CAUD	Q5DN15 bacteriophag
26	33	82.5	222 2 Q4NZU2_9DELT	Q4NZU2 anaeromyxob
27	33	82.5	290 2 Q4LYE1_9BTRK	Q4LYE1 burkholderi
28	33	82.5	359 2 Q67J94_SYNTH	Q67J94 symbiodact
29	33	82.5	409 2 Q8FRQ9_CORBP	Q8FRQ9 corynebacte
30	33	82.5	504 2 Q4NVJ7_9DELT	Q4NVJ7 anaeromyxob
31	33	82.5	576 2 Q551Q1_CRYNE	Q551Q1 cryptococcu

32	33	82.5	667 2 Q5KC26_CRYNE	Q5KC26 cryptococcu
33	33	82.5	696 2 Q4LML8_9BTRK	Q4LML8 burkholderi
34	33	82.5	698 2 Q57X86_9TRYP	Q57X86 trypanosoma
35	33	82.5	1122 2 Q4NQW1_9DELT	Q4NQW1 anaeromyxob
36	33	82.5	1178 2 Q5VOJ0_ORYSA	Q5VOJ0 oryza sativ
37	32	80.0	68 2 Q5O1B5_TERRU	Q5O1B5 tetradon f
38	32	80.0	68 2 Q4RX13_TETNG	Q4RX13 tetradon n
39	32	80.0	86 2 Q89ME5_BRADJ	Q89ME5 bradyrhizob
40	32	80.0	101 2 Q4LUI9_9BTRK	Q4LUI9 burkholderi
41	32	80.0	110 2 Q94J97_ORYSA	Q94J97 oryza sativ
42	32	80.0	137 2 P91989_CAERL	P91989 caenorhabdi
43	32	80.0	144 2 Q53CQ0_9GAMA	Q53CQ0 maeccia fusc
44	32	80.0	177 2 Q6ZDF1_BURMA	Q6ZDF1 burkholderi
45	32	80.0	209 2 P73834_SYNY3	P73834 synchocyst

## ALIGNMENTS

RESULT 1	SIM2 HUMAN	STANDARD	PRT: 667 AA.
ID: SIM2 HUMAN	Q14150; Q60766; Q15470; Q15471; Q15472; Q15473; Q16532;		
AC	Q14150; Q60766; Q15470; Q15471; Q15472; Q15473; Q16532;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DB	Single-minded homolog 2.		
GN	Name=SIM2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA] (ISOFORMS SIM2 AND SIM3).		
RX	MEDLINE=97343329; PubMed=919934;		
RA	Christ R., Scott H.S., Chen H., Kudoh J., Rossier C., Minoshima S.,		
RA	Wang Y., Shimizu N., Antonarakis S.B.;		
RT	"Cloning of two human homologs of the Drosophila single-minded gene		
RT	SIM1 on chromosome 6q and SIM2 on 21q within the Down syndrome		
RT	chromosomal region."		
RL	Genome Res. 7:615-624 (1997).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Shibuya K., Kudoh J., Minoshima S., Kawasaki K., Nakatoh E.,		
RA	Shintani A., Asakawa S., Shimizu N.;		
RT	"Genomic sequencing of 1.2-Mb region on human chromosome 21q22.2."		
RT	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RX	MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;		
RA	Hatori W., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,		
RA	Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,		
RA	Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,		
RA	Pollay A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,		
RA	Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,		
RA	Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,		
RA	Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.B.,		
RA	Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,		
RA	Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,		
RA	Ramer J., Beck A., Klages S., Hennig S., Resselmann L., Dagand E.,		
RA	Wahrner S., Borzym K., Gardner K., Nizetic D., Francis F.,		
RT	Lehrach H., Reinhardt R., Yaspo M.-L.;		
RT	"The DNA sequence of human chromosome 21."		
RL	Nature 405:311-319 (2000).		
RN	[4]		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-247.		
RX	PubMed=8905236;		
RA	Okano S., Kato Y., Nishimura Y., Soeda E.;		
RT	"A 19-kb CpG island associated with single-minded gene 2 in Down		
RT	syndrome chromosomal region."		
RL	DNA Res. 3:175-179 (1996).		
RN	[5]		

RP NUCLEOTIDE SEQUENCE OF 1-58; 87-152; 183-247 AND 249-283.  
 RX MEDLINE=95375794; PubMed=7647800;  
 RA Chen H., Chrest R., Roessler C., Goss A., Antonarakis S.E., Kudoh J.,  
 RT Yamaki A., Shindoh N., Maeda H., Minoshima S., Shimizu N.;  
 RU "Single-minded and Down syndrome?";  
 RL Nat. Genet. 10:9-10(1995).  
 [6]  
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 64-526.  
 RC TISSUE=Fetal brain, and Muscle;  
 RX MEDLINE=98163741; PubMed=9503011; DOI=10.1006/geno.1997.5146;  
 RA Dahmane N., Alt Ghezala G., Gossel P., Chamoun Z.,  
 RA Dufresne-Zacharia M.-C., Lopes C., Rabatel N., Gassanova-Maugendre S.,  
 RA Chetoui Z., Abramowski V., Fayer E., Yasso M.-L., Korn B.,  
 RA Blouin J.-L., Lehrach H., Pouetka A., Antonarakis S.E., Sine P.-M.,  
 RA Creau N., Delabar J.-M.;  
 RT "Transcriptional map of the 2.5-Mb CBR-ERG region of chromosome 21  
 involved in Down syndrome.";  
 RL Genomics 48:12-23(1998).  
 [7]  
 RP NUCLEOTIDE SEQUENCE OF 87-116.  
 RX MEDLINE=96016135; PubMed=7568099;  
 RA Dahmane N., Charron G., Lopes C., Yasso M.-L., Maunoury C.,  
 RA Decotte L., Sine P.-M., Bloch B., Delabar J.M.;  
 RT "Down syndrome-critical region contains a gene homologous to  
 Drosophila sim expressed during rat and human central nervous system  
 development.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9191-9195(1995).  
 [8]  
 RP NUCLEOTIDE SEQUENCE OF 154-181.  
 RX MEDLINE=9629750; PubMed=661114; DOI=10.1006/geno.1996.0332;  
 RA Yamaki A., Noda S., Kudoh J., Shindoh N., Maeda H., Minoshima S.,  
 RA Kawasaki K., Shimizu Y., Shimizu N.;  
 RT "The mammalian single-minded (SIM) gene: mouse cDNA structure and  
 differential expression indicate a candidate gene for Down syndrome.";  
 RL Genomics 35:136-143(1996).  
 [9]  
 RP SUBCELLULAR LOCATION, NUCLEAR LOCALIZATION SIGNAL, AND MUTAGENESIS OF  
 KIP  
 RX PubMed=14697214; DOI=10.1016/j.birc.2003.11.168;  
 RA Kamaki A., Kudoh J., Shimizu N., Shimizu Y.;  
 RT "A novel nuclear localization signal in the human single-minded  
 protein SIM1 and SIM2.";  
 RL Biochem. Biophys. Res. Commun. 313:482-488(2004);  
 CC -1- FUNCTION: Transcription factor that may be a master gene of CNS  
 development in cooperation with Arnt. It may have pleiotropic  
 effects in the tissues expressed during development.  
 CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another  
 bHLH protein. Heterodimer of SIM2 and ARNT.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=SIM2;  
 CC IsoId=Q14190-1; Sequence=Displayed;  
 CC Name=SIM2S;  
 CC IsoId=Q14190-2; Sequence=VSP\_012767;  
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.  
 CC -1- SIMILARITY: Contains 1 PAS (PAS-associated C-terminal) domain.  
 CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) domains.  
 CC -1- SIMILARITY: Contains 1 Single-minded C-terminal domain.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; U80456; AAB62396.1; -; mRNA.  
 CC EMBL; U80457; AAB62397.1; -; mRNA.  
 CC EMBL; AB003185; BAA21489.1; -; Genomic DNA.  
 CC EMBL; AB003185; BAA21490.1; -; Genomic DNA.  
 CC EMBL; AP000697; BAA84433.1; -; Genomic DNA.  
 CC EMBL; AP001726; -; NOT ANNOTATED CDS; Genomic DNA.  
 CC EMBL; D85922; BAA12919.1; -; Genomic DNA.

DR EMBL; D44444; BAA07906.1; -; Genomic DNA.  
 DR EMBL; D44445; BAA07907.1; -; Genomic DNA.  
 DR EMBL; D44446; BAA07908.1; -; Genomic DNA.  
 DR EMBL; D44447; BAA07909.1; -; Genomic DNA.  
 DR EMBL; D44448; BAA07910.1; -; Genomic DNA.  
 DR EMBL; A1001858; CA05055.1; -; mRNA.  
 DR EMBL; X84790; CA55261.1; -; mRNA.  
 DR EMBL; D70838; BAA11108.1; -; Genomic DNA.  
 DR PIR; A58520; A58520.  
 DR PIR; I78525; I78525.  
 DR PIR; I78526; I78526.  
 DR TRANSFAC; T04910; -;  
 DR HGENC; ENSG00000159263; Homo sapiens.  
 DR HGENC; HGENC:10883; SIM2.  
 DR MIM; 600892; -;  
 DR GO; GO:0003700; F:transcription factor activity; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.  
 DR InterPro; IPR001092; HLH basic.  
 DR InterPro; IPR001067; Nuc\_translocat.  
 DR InterPro; IPR001610; PAS.  
 DR InterPro; IPR000014; PAS.  
 DR InterPro; IPR000700; PAS-associ\_C.  
 DR Pfam; PF00010; HLM; 1.  
 DR Pfam; PF00989; PAS; 1.  
 DR Pfam; PF06621; SIM\_C; 1.  
 DR PRINTS; PR00785; NCTRNSLOCATR.  
 DR SMART; SM00353; HLH; 1.  
 DR SMART; SM00086; PAS; 1.  
 DR SMART; SM00091; PAS; 2.  
 DR PROSITE; PS00888; HLM; 1.  
 DR PROSITE; PS50113; PAS; FALSE\_NEG.  
 DR PROSITE; PS50112; PAS; 2.  
 DR KX DNA-binding; Neurogenesis; Development;  
 DR KX Alternative splicing; Nuclear protein; Repeat; Transcription;  
 DR KX Transcription regulation.  
 DR FT DOMAIN 14 54  
 DR FT DOMAIN 77 149  
 DR FT DOMAIN 218 288  
 DR FT DOMAIN 292 335  
 DR FT DOMAIN 358 661  
 DR FT DNA BIND 1 13  
 DR FT MOTIF 367 386  
 DR FT VARSPLIC 526 570  
 DR FT VARSPLIC 571 667  
 DR FT MUTAGEN 367 367  
 DR FT MUTAGEN 368 368  
 DR FT MUTAGEN 369 369  
 DR FT MUTAGEN 370 370  
 DR FT MUTAGEN 371 371  
 DR FT MUTAGEN 372 372  
 DR FT MUTAGEN 373 373  
 DR FT MUTAGEN 375 375  
 DR FT MUTAGEN 376 376  
 DR FT MUTAGEN 377 377  
 DR FT MUTAGEN 378 378  
 DR FT MUTAGEN 379 379  
 DR FT MUTAGEN 380 380  
 DR FT MUTAGEN 381 381  
 DR FT MUTAGEN 382 382  
 DR FT MUTAGEN 383 383  
 DR FT MUTAGEN 385 385  
 DR FT MUTAGEN 386 386  
 DR FT MUTAGEN 387 387  
 DR FT MUTAGEN 388 388  
 DR FT MUTAGEN 389 389  
 DR FT MUTAGEN 390 390  
 DR FT MUTAGEN 391 391  
 DR FT MUTAGEN 392 392  
 DR FT MUTAGEN 393 393  
 DR FT MUTAGEN 394 394  
 DR FT MUTAGEN 395 395  
 DR FT MUTAGEN 396 396  
 DR FT MUTAGEN 397 397  
 DR FT MUTAGEN 398 398  
 DR FT MUTAGEN 399 399  
 DR FT MUTAGEN 400 400  
 DR FT MUTAGEN 401 401  
 DR FT MUTAGEN 402 402  
 DR FT MUTAGEN 403 403  
 DR FT MUTAGEN 404 404  
 DR FT MUTAGEN 405 405  
 DR FT MUTAGEN 406 406  
 DR FT MUTAGEN 407 407  
 DR FT MUTAGEN 408 408  
 DR FT MUTAGEN 409 409  
 DR FT MUTAGEN 410 410  
 DR FT MUTAGEN 411 411  
 DR FT MUTAGEN 412 412  
 DR FT MUTAGEN 413 413  
 DR FT MUTAGEN 414 414  
 DR FT MUTAGEN 415 415  
 DR FT MUTAGEN 416 416  
 DR FT MUTAGEN 417 417  
 DR FT MUTAGEN 418 418  
 DR FT MUTAGEN 419 419  
 DR FT MUTAGEN 420 420  
 DR FT MUTAGEN 421 421  
 DR FT MUTAGEN 422 422  
 DR FT MUTAGEN 423 423  
 DR FT MUTAGEN 424 424  
 DR FT MUTAGEN 425 425  
 DR FT MUTAGEN 426 426  
 DR FT MUTAGEN 427 427  
 DR FT MUTAGEN 428 428  
 DR FT MUTAGEN 429 429  
 DR FT MUTAGEN 430 430  
 DR FT MUTAGEN 431 431  
 DR FT MUTAGEN 432 432  
 DR FT MUTAGEN 433 433  
 DR FT MUTAGEN 434 434  
 DR FT MUTAGEN 435 435  
 DR FT MUTAGEN 436 436  
 DR FT MUTAGEN 437 437  
 DR FT MUTAGEN 438 438  
 DR FT MUTAGEN 439 439  
 DR FT MUTAGEN 440 440  
 DR FT MUTAGEN 441 441  
 DR FT MUTAGEN 442 442  
 DR FT MUTAGEN 443 443  
 DR FT MUTAGEN 444 444  
 DR FT MUTAGEN 445 445  
 DR FT MUTAGEN 446 446  
 DR FT MUTAGEN 447 447  
 DR FT MUTAGEN 448 448  
 DR FT MUTAGEN 449 449  
 DR FT MUTAGEN 450 450  
 DR FT MUTAGEN 451 451  
 DR FT MUTAGEN 452 452  
 DR FT MUTAGEN 453 453  
 DR FT MUTAGEN 454 454  
 DR FT MUTAGEN 455 455  
 DR FT MUTAGEN 456 456  
 DR FT MUTAGEN 457 457  
 DR FT MUTAGEN 458 458  
 DR FT MUTAGEN 459 459  
 DR FT MUTAGEN 460 460  
 DR FT MUTAGEN 461 461  
 DR FT MUTAGEN 462 462  
 DR FT MUTAGEN 463 463  
 DR FT MUTAGEN 464 464  
 DR FT MUTAGEN 465 465  
 DR FT MUTAGEN 466 466  
 DR FT MUTAGEN 467 467  
 DR FT MUTAGEN 468 468  
 DR FT MUTAGEN 469 469  
 DR FT MUTAGEN 470 470  
 DR FT MUTAGEN 471 471  
 DR FT MUTAGEN 472 472  
 DR FT MUTAGEN 473 473  
 DR FT MUTAGEN 474 474  
 DR FT MUTAGEN 475 475  
 DR FT MUTAGEN 476 476  
 DR FT MUTAGEN 477 477  
 DR FT MUTAGEN 478 478  
 DR FT MUTAGEN 479 479  
 DR FT MUTAGEN 480 480  
 DR FT MUTAGEN 481 481  
 DR FT MUTAGEN 482 482  
 DR FT MUTAGEN 483 483  
 DR FT MUTAGEN 484 484  
 DR FT MUTAGEN 485 485  
 DR FT MUTAGEN 486 486  
 DR FT MUTAGEN 487 487  
 DR FT MUTAGEN 488 488  
 DR FT MUTAGEN 489 489  
 DR FT MUTAGEN 490 490  
 DR FT MUTAGEN 491 491  
 DR FT MUTAGEN 492 492  
 DR FT MUTAGEN 493 493  
 DR FT MUTAGEN 494 494  
 DR FT MUTAGEN 495 495  
 DR FT MUTAGEN 496 496  
 DR FT MUTAGEN 497 497  
 DR FT MUTAGEN 498 498  
 DR FT MUTAGEN 499 499  
 DR FT MUTAGEN 500 500  
 DR FT MUTAGEN 501 501  
 DR FT MUTAGEN 502 502  
 DR FT MUTAGEN 503 503  
 DR FT MUTAGEN 504 504  
 DR FT MUTAGEN 505 505  
 DR FT MUTAGEN 506 506  
 DR FT MUTAGEN 507 507  
 DR FT MUTAGEN 508 508  
 DR FT MUTAGEN 509 509  
 DR FT MUTAGEN 510 510  
 DR FT MUTAGEN 511 511  
 DR FT MUTAGEN 512 512  
 DR FT MUTAGEN 513 513  
 DR FT MUTAGEN 514 514  
 DR FT MUTAGEN 515 515  
 DR FT MUTAGEN 516 516  
 DR FT MUTAGEN 517 517  
 DR FT MUTAGEN 518 518  
 DR FT MUTAGEN 519 519  
 DR FT MUTAGEN 520 520  
 DR FT MUTAGEN 521 521  
 DR FT MUTAGEN 522 522  
 DR FT MUTAGEN 523 523  
 DR FT MUTAGEN 524 524  
 DR FT MUTAGEN 525 525  
 DR FT MUTAGEN 526 526  
 DR FT MUTAGEN 527 527  
 DR FT MUTAGEN 528 528  
 DR FT MUTAGEN 529 529  
 DR FT MUTAGEN 530 530  
 DR FT MUTAGEN 531 531  
 DR FT MUTAGEN 532 532  
 DR FT MUTAGEN 533 533  
 DR FT MUTAGEN 534 534  
 DR FT MUTAGEN 535 535  
 DR FT MUTAGEN 536 536  
 DR FT MUTAGEN 537 537  
 DR FT MUTAGEN 538 538  
 DR FT MUTAGEN 539 539  
 DR FT MUTAGEN 540 540  
 DR FT MUTAGEN 541 541  
 DR FT MUTAGEN 542 542  
 DR FT MUTAGEN 543 543  
 DR FT MUTAGEN 544 544  
 DR FT MUTAGEN 545 545  
 DR FT MUTAGEN 546 546  
 DR FT MUTAGEN 547 547  
 DR FT MUTAGEN 548 548  
 DR FT MUTAGEN 549 549  
 DR FT MUTAGEN 550 550  
 DR FT MUTAGEN 551 551  
 DR FT MUTAGEN 552 552  
 DR FT MUTAGEN 553 553  
 DR FT MUTAGEN 554 554  
 DR FT MUTAGEN 555 555  
 DR FT MUTAGEN 556 556  
 DR FT MUTAGEN 557 557  
 DR FT MUTAGEN 558 558  
 DR FT MUTAGEN 559 559  
 DR FT MUTAGEN 560 560  
 DR FT MUTAGEN 561 561  
 DR FT MUTAGEN 562 562  
 DR FT MUTAGEN 563 563  
 DR FT MUTAGEN 564 564  
 DR FT MUTAGEN 565 565  
 DR FT MUTAGEN 566 566  
 DR FT MUTAGEN 567 567  
 DR FT MUTAGEN 568 568  
 DR FT MUTAGEN 569 569  
 DR FT MUTAGEN 570 570  
 DR FT MUTAGEN 571 571  
 DR FT MUTAGEN 572 572  
 DR FT MUTAGEN 573 573  
 DR FT MUTAGEN 574 574  
 DR FT MUTAGEN 575 575  
 DR FT MUTAGEN 576 576  
 DR FT MUTAGEN 577 577  
 DR FT MUTAGEN 578 578  
 DR FT MUTAGEN 579 579  
 DR FT MUTAGEN 580 580  
 DR FT MUTAGEN 581 581  
 DR FT MUTAGEN 582 582  
 DR FT MUTAGEN 583 583  
 DR FT MUTAGEN 584 584  
 DR FT MUTAGEN 585 585  
 DR FT MUTAGEN 586 586  
 DR FT MUTAGEN 587 587  
 DR FT MUTAGEN 588 588  
 DR FT MUTAGEN 589 589  
 DR FT MUTAGEN 590 590  
 DR FT MUTAGEN 591 591  
 DR FT MUTAGEN 592 592  
 DR FT MUTAGEN 593 593  
 DR FT MUTAGEN 594 594  
 DR FT MUTAGEN 595 595  
 DR FT MUTAGEN 596 596  
 DR FT MUTAGEN 597 597  
 DR FT MUTAGEN 598 598  
 DR FT MUTAGEN 599 599  
 DR FT MUTAGEN 600 600  
 DR FT MUTAGEN 601 601  
 DR FT MUTAGEN 602 602  
 DR FT MUTAGEN 603 603  
 DR FT MUTAGEN 604 604  
 DR FT MUTAGEN 605 605  
 DR FT MUTAGEN 606 606  
 DR FT MUTAGEN 607 607  
 DR FT MUTAGEN 608 608  
 DR FT MUTAGEN 609 609  
 DR FT MUTAGEN 610 610  
 DR FT MUTAGEN 611 611  
 DR FT MUTAGEN 612 612  
 DR FT MUTAGEN 613 613  
 DR FT MUTAGEN 614 614  
 DR FT MUTAGEN 615 615  
 DR FT MUTAGEN 616 616  
 DR FT MUTAGEN 617 617  
 DR FT MUTAGEN 618 618  
 DR FT MUTAGEN 619 619  
 DR FT MUTAGEN 620 620  
 DR FT MUTAGEN 621 621  
 DR FT MUTAGEN 622 622  
 DR FT MUTAGEN 623 623  
 DR FT MUTAGEN 624 624  
 DR FT MUTAGEN 625 625  
 DR FT MUTAGEN 626 626  
 DR FT MUTAGEN 627 627  
 DR FT MUTAGEN 628 628  
 DR FT MUTAGEN 629 629  
 DR FT MUTAGEN 630 630  
 DR FT MUTAGEN 631 631  
 DR FT MUTAGEN 632 632  
 DR FT MUTAGEN 633 633  
 DR FT MUTAGEN 634 634  
 DR FT MUTAGEN 635 635  
 DR FT MUTAGEN 636 636  
 DR FT MUTAGEN 637 637  
 DR FT MUTAGEN 638 638  
 DR FT MUTAGEN 639 639  
 DR FT MUTAGEN 640 640  
 DR FT MUTAGEN 641 641  
 DR FT MUTAGEN 642 642  
 DR FT MUTAGEN 643 643  
 DR FT MUTAGEN 644 644  
 DR FT MUTAGEN 645 645  
 DR FT MUTAGEN 646 646  
 DR FT MUTAGEN 647 647  
 DR FT MUTAGEN 648 648  
 DR FT MUTAGEN 649 649  
 DR FT MUTAGEN 650 650  
 DR FT MUTAGEN 651 651  
 DR FT MUTAGEN 652 652  
 DR FT MUTAGEN 653 653  
 DR FT MUTAGEN 654 654  
 DR FT MUTAGEN 655 655  
 DR FT MUTAGEN 656 656  
 DR FT MUTAGEN 657 657  
 DR FT MUTAGEN 658 658  
 DR FT MUTAGEN 659 659  
 DR FT MUTAGEN 660 660  
 DR FT MUTAGEN 661 661  
 DR FT MUTAGEN 662 662  
 DR FT MUTAGEN 663 663  
 DR FT MUTAGEN 664 664  
 DR FT MUTAGEN 665 665  
 DR FT MUTAGEN 666 666  
 DR FT MUTAGEN 667 667  
 DR FT MUTAGEN 668 668  
 DR FT MUTAGEN 669 669  
 DR FT MUTAGEN 670 670  
 DR FT MUTAGEN 671 671  
 DR FT MUTAGEN 672 672  
 DR FT MUTAGEN 673 673  
 DR FT MUTAGEN 674 674  
 DR FT MUTAGEN 675 675  
 DR FT MUTAGEN 676 676  
 DR FT MUTAGEN 677 677  
 DR FT MUTAGEN 678 678  
 DR FT MUTAGEN 679 679  
 DR FT MUTAGEN 680 680  
 DR FT MUTAGEN 681 681  
 DR FT MUTAGEN 682 682  
 DR FT MUTAGEN 683 683  
 DR FT MUTAGEN 684 684  
 DR FT MUTAGEN 685 685  
 DR FT MUTAGEN 686 686  
 DR FT MUTAGEN 687 687  
 DR FT MUTAGEN 688 688  
 DR FT MUTAGEN 689 689  
 DR FT MUTAGEN 690 690  
 DR FT MUTAGEN 691 691  
 DR FT MUTAGEN 692 692  
 DR FT MUTAGEN 693 693  
 DR FT MUTAGEN 694 694  
 DR FT MUTAGEN 695 695  
 DR FT MUTAGEN 696 696  
 DR FT MUTAGEN 697 697  
 DR FT MUTAGEN 698 698  
 DR FT MUTAGEN 699 699  
 DR FT MUTAGEN 700 700  
 DR FT MUTAGEN 701 701  
 DR FT MUTAGEN 702 702  
 DR FT MUTAGEN 703 703  
 DR FT MUTAGEN 704 704  
 DR FT MUTAGEN 705 705  
 DR FT MUTAGEN 706 706  
 DR FT MUTAGEN 707 707  
 DR FT MUTAGEN 708 708  
 DR FT MUTAGEN 709 709  
 DR FT MUTAGEN 710 710  
 DR FT MUTAGEN 711 711  
 DR FT MUTAGEN 712 712  
 DR FT MUTAGEN 713 713  
 DR FT MUTAGEN 714 714  
 DR FT MUTAGEN 715 715  
 DR FT MUTAGEN 716 716  
 DR FT MUTAGEN 717 717  
 DR FT MUTAGEN 718 718  
 DR FT MUTAGEN 719 719  
 DR FT MUTAGEN 720 720  
 DR FT MUTAGEN 721 721  
 DR FT MUTAGEN 722 722  
 DR FT MUTAGEN 723 723  
 DR FT MUTAGEN 724 724  
 DR FT MUTAGEN 725 725  
 DR FT MUTAGEN 726 726  
 DR FT MUTAGEN 727 727  
 DR FT MUTAGEN 728 728  
 DR FT MUTAGEN 729 729  
 DR FT MUTAGEN 730 730  
 DR FT MUTAGEN 731 731  
 DR FT MUTAGEN 732 732  
 DR FT MUTAGEN 733 733  
 DR FT MUTAGEN 734 734  
 DR FT MUTAGEN 735 735  
 DR FT MUTAGEN 736 736  
 DR FT MUTAGEN 737 737  
 DR FT MUTAGEN 738 738  
 DR FT MUTAGEN 739 739  
 DR FT MUTAGEN 740 740  
 DR FT MUTAGEN 741 741  
 DR FT MUTAGEN 742 742  
 DR FT MUTAGEN 743 743  
 DR FT MUTAGEN 744 744  
 DR FT MUTAGEN 745 745  
 DR FT MUTAGEN 746 746  
 DR FT MUTAGEN 747 747  
 DR FT MUTAGEN 748 748  
 DR FT MUTAGEN 749 749  
 DR FT MUTAGEN 750 750  
 DR FT MUTAGEN 751 751  
 DR FT MUTAGEN 752 752  
 DR FT MUTAGEN 753 753  
 DR FT MUTAGEN 754 754  
 DR FT MUTAGEN 755 755  
 DR FT MUTAGEN 756 756  
 DR FT MUTAGEN 757 757  
 DR FT MUTAGEN 758 758  
 DR FT MUTAGEN 759 759  
 DR FT MUTAGEN 760 760  
 DR FT MUTAGEN 761 761  
 DR FT MUTAGEN 762 762  
 DR FT MUTAGEN 763 763  
 DR FT MUTAGEN 764 764  
 DR FT MUTAGEN 765 765  
 DR FT MUTAGEN 766 766  
 DR FT MUTAGEN 767 767  
 DR FT MUTAGEN 768 768  
 DR FT MUTAGEN 769 769  
 DR FT MUTAGEN 770 770  
 DR FT MUTAGEN 771 771  
 DR FT MUTAGEN 772 772  
 DR FT MUTAGEN 773 773  
 DR FT MUTAGEN 774 774  
 DR FT MUTAGEN 775 775  
 DR FT MUTAGEN 776 776  
 DR FT MUTAGEN 777 777  
 DR FT MUTAGEN 778 778  
 DR FT MUTAGEN 779 779  
 DR FT MUTAGEN 780 780  
 DR FT MUTAGEN 781 781  
 DR FT MUTAGEN 782 782  
 DR FT MUTAGEN 783 783  
 DR FT MUTAGEN 784 784  
 DR FT MUTAGEN 785 785  
 DR FT MUTAGEN 786 786  
 DR FT MUTAGEN 787 787  
 DR FT MUTAGEN 788 788  
 DR FT MUTAGEN 789 789  
 DR FT MUTAGEN 790 790  
 DR FT MUTAGEN 791 791  
 DR FT MUTAGEN 792 792  
 DR FT MUTAGEN 793 793  
 DR FT MUTAGEN 794 794  
 DR FT MUTAGEN 795 795  
 DR FT MUTAGEN 796 796  
 DR FT MUTAGEN 797 797  
 DR FT MUTAGEN 798 798  
 DR FT MUTAGEN 799 799  
 DR FT MUTAGEN 800 800  
 DR FT MUTAGEN 801 801  
 DR FT MUTAGEN 802 802  
 DR FT MUTAGEN 803 803  
 DR FT MUTAGEN 804 804  
 DR FT MUTAGEN 805 805  
 DR FT MUTAGEN 806 806  
 DR FT MUTAGEN 807 807  
 DR FT MUTAGEN 808 808  
 DR FT MUTAGEN 809 809  
 DR FT MUTAGEN 810 810  
 DR FT MUTAGEN 811 811  
 DR FT MUTAGEN 812 812  
 DR FT MUTAGEN 813 813  
 DR FT MUTAGEN 814 814  
 DR FT MUTAGEN 815 815  
 DR FT MUTAGEN 816 816  
 DR FT MUTAGEN 817 817  
 DR FT MUTAGEN 818 818  
 DR FT MUTAGEN 819 819  
 DR FT MUTAGEN 820 820  
 DR FT MUTAGEN 821 821  
 DR FT MUTAGEN 822 822  
 DR FT MUTAGEN 823 823  
 DR FT MUTAGEN 824 824  
 DR FT MUTAGEN 825 825  
 DR FT MUTAGEN 826 826  
 DR FT MUTAGEN 827 827  
 DR FT MUTAGEN 828 828  
 DR FT MUTAGEN 829 829  
 DR FT MUTAGEN 830 830  
 DR FT MUTAGEN 831 831  
 DR FT MUTAGEN 832 832  
 DR FT MUTAGEN 833 833  
 DR FT MUTAGEN 834 834  
 DR FT MUTAGEN 835 835  
 DR FT MUTAGEN 836 836  
 DR FT MUTAGEN 837 837  
 DR FT MUTAGEN 838 838  
 DR FT MUTAGEN 839 839  
 DR FT MUTAGEN 840 840  
 DR FT MUTAGEN 841 841  
 DR FT MUTAGEN 842 842  
 DR FT MUTAGEN 843 843  
 DR FT MUTAGEN 844 844  
 DR FT MUTAGEN 845 845  
 DR FT MUTAGEN 846 846  
 DR FT MUTAGEN 847 847  
 DR FT MUTAGEN 848 848  
 DR FT MUTAGEN 849 849  
 DR FT MUTAGEN 850 850  
 DR FT MUTAGEN 851 851  
 DR FT MUTAGEN 852 852  
 DR FT MUTAGEN 853 853  
 DR FT MUTAGEN 854 854  
 DR FT MUTAGEN 855 855  
 DR FT MUTAGEN 856 856  
 DR FT MUTAGEN 857 857  
 DR FT MUTAGEN 858 858  
 DR FT MUTAGEN 859 859  
 DR FT MUTAGEN 860 860  
 DR FT MUTAGEN 861 861  
 DR FT MUTAGEN 862 862  
 DR FT MUTAGEN 863 863  
 DR FT MUTAGEN 864 864  
 DR FT MUTAGEN 865 865  
 DR FT MUTAGEN 866 866  
 DR FT MUTAGEN 867 867  
 DR FT MUTAGEN 868 868  
 DR FT MUTAGEN 869 869  
 DR FT MUTAGEN 870 870  
 DR FT MUTAGEN 871 871  
 DR FT MUTAGEN 872 872  
 DR FT MUTAGEN 873 873  
 DR FT MUTAGEN 874 874  
 DR FT MUTAGEN 875 875  
 DR FT MUTAGEN 876 876  
 DR FT MUTAGEN 877 877  
 DR FT MUTAGEN 878 878  
 DR FT MUTAGEN 879 879  
 DR FT MUTAGEN 880 880  
 DR FT MUTAGEN 881 881  
 DR FT MUTAGEN 882 882  
 DR FT MUTAGEN 883 883  
 DR FT MUTAGEN 884 884  
 DR FT MUTAGEN 885 885  
 DR FT MUTAGEN 886 886  
 DR FT MUTAGEN 887 887  
 DR FT MUTAGEN 888 888  
 DR FT MUTAGEN 889 889  
 DR FT MUTAGEN 890 890  
 DR FT MUTAGEN 891 891  
 DR FT MUTAGEN 892 892  
 DR FT MUTAGEN 893 893  
 DR FT MUTAGEN 894 894  
 DR FT MUTAGEN 895 895  
 DR FT MUTAGEN 896 896  
 DR FT MUTAGEN 897 897  
 DR FT MUTAGEN 898 898  
 DR FT MUTAGEN 899 899  
 DR FT MUTAGEN 900 900  
 DR FT MUTAGEN 901 901  
 DR FT MUTAGEN 902 902  
 DR FT MUTAGEN 903 903  
 DR FT MUTAGEN 904 904  
 DR FT MUTAGEN 905 905  
 DR FT MUTAGEN 906 906  
 DR FT MUTAGEN 907 907  
 DR FT MUTAGEN 908 908  
 DR FT MUTAGEN 909 909  
 DR FT MUTAGEN 910 910  
 DR FT MUTAGEN 911 911  
 DR FT MUTAGEN 912 912  
 DR FT MUTAGEN 913 913  
 DR FT MUTAGEN 914 914  
 DR FT MUTAGEN 915 915  
 DR FT MUTAGEN 916 916  
 DR FT MUTAGEN 917 917  
 DR FT MUTAGEN 918 918  
 DR FT MUTAGEN 919 919  
 DR FT MUTAGEN 920 920  
 DR FT MUTAGEN 921 921  
 DR FT MUTAGEN 922 922  
 DR FT MUTAGEN 923 923  
 DR FT MUTAGEN 924 924  
 DR FT MUTAGEN 925 925  
 DR FT MUTAGEN 926 926  
 DR FT MUTAGEN 927 927  
 DR FT MUTAGEN 928 928  
 DR FT MUTAGEN 929 929  
 DR FT MUTAGEN 930 930  
 DR FT MUTAGEN 931 931  
 DR FT MUTAGEN 932 932  
 DR FT MUTAGEN 933 933  
 DR FT MUTAGEN 934 934  
 DR FT MUTAGEN 935 935  
 DR FT MUTAGEN 936 936  
 DR FT MUTAGEN 937 937  
 DR FT MUTAGEN 938 938  
 DR FT MUTAGEN 939 939  
 DR FT MUTAGEN 940 940  
 DR FT MUTAGEN 941 941  
 DR FT MUTAGEN 942 942  
 DR FT MUTAGEN 943 943  
 DR FT MUTAGEN 944 944  
 DR FT MUTAGEN 945 945  
 DR FT MUTAGEN 946 946  
 DR FT MUTAGEN 947 947  
 DR FT MUTAGEN 948 948  
 DR FT MUTAGEN 949 949  
 DR FT MUTAGEN 950 950  
 DR FT MUTAGEN 951 951  
 DR FT MUTAGEN 952 952  
 DR FT MUTAGEN 953 953  
 DR FT MUTAGEN 954 954  
 DR FT MUTAGEN 955 955  
 DR FT MUTAGEN 956 956  
 DR FT MUTAGEN 957 957  
 DR FT MUTAGEN 958 958  
 DR FT MUTAGEN 959 959  
 DR FT MUTAGEN 960 960  
 DR FT MUTAGEN 961 961  
 DR FT MUTAGEN 962 962  
 DR FT MUTAGEN 963 963  
 DR FT MUTAGEN 964 964  
 DR FT MUTAGEN 965 965  
 DR FT MUTAGEN 966 966  
 DR FT MUTAGEN 967 967  
 DR FT MUTAGEN 968 968  
 DR FT MUTAGEN 969 969  
 DR FT MUTAGEN 970 970  
 DR FT

Query Match 100.0%; Score 40; DB 1; Length 667;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
 Db 558 AKARQAR 566

## RESULT 2

Q92X88 RHIME PRELIMINARY; PRT; 80 AA.  
 AC Q92X88;  
 DT 01-DEC-2001 (TRENBLREL. 19, Created)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
 DE Hypothetical protein SMO20074.  
 GN OrderedLocusNames=RB0074; ORFNames=SMO20074;  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Plasmid pSymB.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 ON NCBI\_TaxID=382;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=1021;  
 RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;  
 RA Fianan T.M., Weidner S., Wong K., Buhmester J., Chai P.,  
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowle A., Gouzy J.,  
 RA Golding B., Pehler A.;  
 RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-  
 RT fixing endosymbiont Sinorhizobium meliloti."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).  
 DR EMBL; AL591985; CAC48474.1; -; Genomic\_DNA.  
 DR PIR; B95851; B95851.  
 KW Complete proteome; Hypothetical protein; Plasmid.  
 SQ SEQUENCE 80 AA; 8935 MW; ED59C74ABAE17932 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 80;  
 Best Local Similarity 88.9%; Pred. No. 20;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
 Db 44 AKARQAR 52

## RESULT 3

O6ZRH9 HUMAN PRELIMINARY; PRT; 516 AA.  
 AC O6ZRH9;  
 DT 05-JUL-2004 (TRENBLREL. 27, Created)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)  
 DE Hypothetical protein FLJ46347.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA TISSUE=Testis;  
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Igono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
 RA Miyakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,  
 RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isegaki T.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK128215; BAC07331.1; -; mRNA.  
 SQ SEQUENCE 516 AA; 53616 MW; 1243677FA7FB3F44 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 516;  
 Best Local Similarity 88.9%; Pred. No. 97;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
 Db 364 AKARQAR 372

## RESULT 4

OSNTN3\_9BACT PRELIMINARY; PRT; 186 AA.  
 AC OSNTN3;  
 DT 01-FEB-2005 (TRENBLREL. 29, Created)  
 DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)  
 DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)  
 DE Hypothetical protein nap3-4.  
 GN Name=nap3-4;  
 OS uncultured bacterium.  
 OC Bacteria; environmental samples.  
 ON NCBI\_TaxID=77133;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=15608629; DOI=10.1038/nbt1048;  
 RA Uchiyama T., Abe T., Ikemura T., Watanabe K.;  
 RT "Substrate-induced gene-expression screening of environmental  
 RT metagenome libraries for isolation of catabolic genes."  
 RL Nat. Biotechnol. 23:88-93(2005).  
 DR EMBL; AB186503; BAD0988.1; -; Genomic\_DNA.  
 DR InterPro; IPR004238; LEA.  
 DR Pfam; PF02987; LEA\_4; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 186 AA; 19238 MW; B67587D5622A37A8 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 186;  
 Best Local Similarity 88.9%; Pred. No. 63;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKARQAR 9  
 Db 80 AKARQAR 88

## RESULT 5

Q4P8F5 USTMA PRELIMINARY; PRT; 562 AA.  
 AC Q4P8F5;  
 DT 13-SEP-2005 (TRENBLREL. 31, Created)  
 DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=UM03608.1;  
 OS Ustilago maydis 521.  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 ON NCBI\_TaxID=237631;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA STRAIN=521;  
 RA Birren B., Nussbaum C., Abebe A., Aboueljelil A., Adekoya E.,  
 RA Alt-zahra M., Allen T., Allen P., Anderson M., Anderson S.,  
 RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,  
 RA Bayul T., Biltsteyn B., Bloom T., Blye J., Boguslavsky L.,  
 RA Bowdley M., Boukhalter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshtsang Y., Citroen M.,  
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
 RA David R., Dawoe T., Degray S., Dodge S., Doolley K., Dorje P.,  
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
 RA Erickson J., Fatina A., Faro S., Ferreira P., Fischer H.,  
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,  
 RA Ghrke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
 RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,